



SEQUENCE LISTING

Gero Miesenbock, et al.

<120> Hybrid Molecules And Their Use For Optically Detecting Changes
In
Cellular Microenvironments

<130> 2955-4004US3

<140> 10/676,428

<141> 2003-09-30

<150> 09/023,946

<151> 1998-02-13

<150> 60/038,179

<151> 1997-02-13

<150> 60/036,805

<151> 1997-02-14

<160> 39

<170> PatentIn version 3.2

<210> 1

<211> 242

<212> PRT

<213> Aequora Victoria

<220>

<221> MISC_FEATURE

<223> green fluorescent protein

<400> 1

Met Gly Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Thr Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly
225 230 235 240

Ser Arg

<210> 2
<211> 729
<212> DNA
<213> Aequora Victoria

<400> 2
atgggtaaag gagaagaact ttctactgga gttgtcccaa ttcttgttga attagatggt
60

gatgttaatg ggcacaaatt ttctgtcagt ggagagggtg aaggatgatgc aacatacggg
120

aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccgaagggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggatga tacccttggt
360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga
480

accaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caagtccgga
720

tctagataa
729

<210> 3
<211> 717
<212> DNA
<213> Aequora Victoria

<400> 3
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggg
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacggg
120

aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggatga tacccttggt
360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataacga tcaccagggtg tacatcatgg cagacaaaca aaagaatgga
480

atcaaagcta acttcaaaat tagacacaac attgaagatg gaggcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 4
<211> 717
<212> DNA
<213> Aequora Victoria

<220>

<221> misc_feature
<223> 14E12t

<400> 4
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttgttga attagatggt
60
gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg
120
aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240
catgactttt tcaagagtgc catgcccgaagggttatgtac aggaaagaac tatatattttc
300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggatga tacccttggt
360
aatagaattg agttaaaagg tattgatattt aaagaagatg gaaacattct tggacacaaa
420
ttggagtaca actataacga tcacgatgtg tacatcatgg cagacaaaca aaagaatggt
480
accaaagcta actttcaagt tcgccacaac attgaagatg gaggcgttca actagcagac
540
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600
ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660
cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 5
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 1D10

<400> 5
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttgttga attagatggt
60
gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg
120
aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240
catgactttt tcaagagtgc catgcccgaagggttatgtac aggaaagaac tatatattttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataacga tcacaatgtg tacatcatgg cagacaaaca aaagaatgga
480

atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 6
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 2F10

<400> 6
atgagtaaag gagaagaact tttcactgga gttgtcccaa ttcttggtga attagatggt
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacgga
120

aaacttacc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataacga tcacatgtg tacatcatgg cagacaaaca aaagaatgga
480

atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 7
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 2H2

<400> 7
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggt
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacggg
120

aaacttacc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatatttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataacga tcacgtgggtg tacatcatgg cagacaaaca aaagaatgga
480

atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 8
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 1B11

<400> 8
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggt
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg
120

aaacttacc c ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataacga tcaccaggtg tacatcatgg cagacaaaca aaagaatgga
480

atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 9
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 8F6

<400> 9
atgagtaaag gagaagaact tttcactgga gttgtcccaa ttcttggtga attagatggg
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg
120

aaacttacc c ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataacga tcacactgtg tacatcatgg cagacaaaca aaagaatgga
480

atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 10

<211> 717

<212> DNA

<213> Aequora Victoria

<220>

<221> misc_feature

<223> 19E10

<400> 10

atgagtaaag gagaagaact tttcactgga gttgtcccaa ttcttgttga attagatggg
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacggg
120

aaacttacc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360

aatagaattg agttaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggagtaca actataacga tcacttggtg tacatcatgg cagacaaaca aaagaatggg
480

accaaagtta actttcaagt tcaccacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 11

<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 14E12

<400> 11
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggg
60
gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacggg
120
aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240
catgactttt tcaagagtgc catgcccgaagggtatgtac aggaaagaac tatatttttc
300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaagggtga tacccttggt
360
aatagaattg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420
ttggagtaca actataacga tcacgatgtg tacatcatgg cagacaaaca aaagaatggg
480
accaaagtta actttcaagt tcgccacaac attgaagatg gaagcgttca actagcagac
540
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600
ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660
cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 12
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 14C9

<400> 12
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggg
60
gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacggg
120
aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240
catgactttt tcaagagtgc catgcccgaagggttatgtac aggaaagaac tatatattttc
300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360
aatagaattg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420
ttggagtaca actataacga tcacctggtg tacatcatgg cagacaaaca aaagaatggt
480
accaaagtta actttcaagt tcgccacaac attgaagatg gaagcgttca actagcagac
540
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600
ctgcacacac aatctgcctt ttcgaaagat cccaacgaaa agagagacca catggtcctt
660
cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 13
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 14C8

<400> 13
atgagtaaag gagaagaact tttcactgga gttgtcccaa ttcttggtga attagatggt
60
gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacgga
120
aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240
catgactttt tcaagagtgc catgcccgaagggttatgtac aggaaagaac tatatattttc
300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360
aatagaattg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420
ttggagtaca actataacct tcactatgtg tacatcatgg cagacaaaca aaagaatggt
480
accaaagtta actttcaagt tcaccacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc tttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 14
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 2G3

<400> 14
atgagtaaag gagaagaact tttcactgga gttgtcccaa ttcttggtga attagatggt
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacggg
120

aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat accagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggatga tacccttggt
360

aatagaatcg agttaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataacga gcacttggtg tacatcatgg cagacaaaca aaagaatggt
480

accaaagcta actttaaaat tcaccacaac attgaagatg gaggcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc tttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 15
<211> 717
<212> DNA
<213> Aequora Victoria

<220>

<221> misc_feature
<223> S202H

<400> 15
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggt
60
gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacgga
120
aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240
catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360
aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420
ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga
480
atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600
ctgcacacac aatctgcctt ttcgaaagat cccaacgaaa agagagacca catggtcctt
660
cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 16
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 14D9

<400> 16
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggt
60
gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacgga
120
aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240
catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaagggtga tacccttggt
360

aatagaattg agttaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggagtaca actataaccc tcactgggtg tacatcatgg cagacaaaca aaagaatggt
480

accaaagtta actttcaagt tcaccacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caataa
717

<210> 17
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> 8H8

<400> 17
atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggt
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggatgatgc aacatacgga
120

aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccgaagggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaagggtga tacccttggt
360

aatagaatcg agttaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa
420

ttggaataca actataaccc tcactgggtg tacatcatgg cagacaaaca aaagaatgga
480

atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
717

<210> 18
<211> 1668
<212> DNA
<213> Cypridina

<220>
<221> misc_feature
<223> Cypridina Luciferase

<400> 18
atgaagataa taattctgtc tggttatattg gcttactgtg tcaccgtcaa ctgtcaagat
60

gcatgtcctg tagaagcgga accgccatca agtacaccaa cagttccaac ttcttgtaga
120

gctaaagaag gagaatgtat agataccaga tgcgcaacat gtaaacgaga tatactatca
180

gaeggactgt gtgaaaataa accaggggaag acatgctgta gaatgtgcca gtatgtgatt
240

gaatgcagag tagaagcagc tggttatttt agaacgtttt acggcaaaaag atttaatttt
300

caggaacctg gtaaatatgt gctggctagg ggaaccaagg gtggcgattg gtctgtaacc
360

ctcaccatgg agaacctaga tggacagaag ggagctgtgc tgactaagac aacctggag
420

gttgcaggag acgtaataga cattactcaa gctactgcag atcctatcac agttaacgga
480

ggagctgacc cagttatcgc taaccggttc acaattgggtg aggtgaccat tgctgttggt
540

gaaataccgg gcttcaatat cacagtcac gaattcttta aactaatcgt gattgatatt
600

ctggggaggaa gatctgtgag aattgctcca gacacagcaa acaaaggact gatatctggt
660

atctgtggta atctggagat gaatgacgct gatgacttta ctacagacgc agatcagctg
720

gcatccaac ccaacataaa caaagagttc gacggctgcc cattctatgg gaatccttct
780

gatatcgaat actgcaaagg tctcatggag ccatacagag ctgtatgtcg taacaatatc
840

aacttctact attacactct atcctgcgcc ttcgcttact gtatgggagg agaagaaaga
900

gctaaacacg tccttttcga ctatgttgag acatgcgctg caccggaac gagaggaacg
960

tgtgttttat caggacatac tttctatgac acattcgaca aagccagata tcaattccag
1020

ggcccatgca aagagcttct gatggccgca gactgttact ggaacacatg ggatgtaaag
1080

gtttcacata gagatgttga gtcatacact gaggtagaga aagtaacaat caggaaacag
1140

tcaactgtag tagatctgat tgtggatggc aagcaggtca aggttggagg agtggatgta
1200

tctatcccg t acagctctga gaacacatcc atatactggc aggatggaga catcctgacg
1260

acggccatcc tacctgaagc tctcgtcgtt aagttcaact ttaagcagct ccttgtagtt
1320

catatcagag atccattcga tggaaagaca tgcggcatat gtggttaacta taatcaagat
1380

tcaactgatg atttctttga cgcagaagga gcatgcgctc tgacccccaa tccccagga
1440

tgtacagagg agcagaaacc agaagctgag cgactctgca atagtctatt tgatagttct
1500

atcgacgaga aatgtaatgt ctgctacaag ccggaccgta ttgcccgatg tatgtacgag
1560

tattgcctga ggggacagca aggattctgt gaccatgctt gggagttcaa gaaagaatgc
1620

tacataaagc atggagacac tctagaagta ccacctgaat gtcaataa
1668

<210> 19
<211> 717
<212> DNA
<213> Aequora Victoria

<220>
<221> misc_feature
<223> C6

<220>
<221> misc_feature
<222> (708)..(708)
<223> n is a, c, g, or t

<400> 19
atgattaaag gagaagaact ttctactgga gttgtcccaa ttcttgttga attagatggt
60

gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg
120

aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
180

gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
240

catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc
300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
360

aatagaatcg agttaaagg tattgatttt aaagatgatg gaaacattct tggacacaaa
420

ttggaatata actataacga gcacttggtg tacatcatgg cagacaaaca aaagaatggt
480

accaaagcta tctttcaagt tcaccacaac attgaagatg gaggcgttca actagcagac
540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac
600

ctgcacacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcttt
660

cttgagtttg taacagctgc tgggattaca catggcatgg atgaagtnta caaataa
717

<210> 20

<211> 238

<212> PRT

<213> Aequora Victoria

<400> 20

Met Ile Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Asp Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Glu His Leu Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly

145		150		155		160									
Thr	Lys	Ala	Ile	Phe	Gln	Val	His	His	Asn	Ile	Glu	Asp	Gly	Gly	Val
				165					170					175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	His	Thr	Gln	Ser	Ala	Leu	Ser
		195					200					205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Phe	Leu	Glu	Phe	Val
	210					215					220				
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Val	Tyr	Lys		
225					230					235					

<210> 21
 <211> 717
 <212> DNA
 <213> Aequora Victoria

<400> 21
 atgagtaaag gagaagaact tttcactgga gttgtcccaa ttcttgttga attagatggt
 60
 gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg
 120
 aaacttacc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt
 180
 gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg
 240
 catgactttt tcaagagtgc catgcccgaagggttatgtac aggaaagaac tatatttttc
 300
 aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttggt
 360
 aatagaatcg agttaaaggg tattgatttt aaagaagatg gaaacattct tggacacaaa
 420
 ttggaataca actataacga tcaccaggtg tacatcatgg cagacaaaca aaagaatgga
 480
 atcaaagcta acttcaaaat tagacacaac attgaagatg gaggcgttca actagcagac
 540
 cattatcaac aaaatactcc aattggcgat gggcccggtcc ttttaccaga caaccattac
 600
 ctgtttacaa cttctactct ttcgaaagat cccaacgaaa agagagacca catggtcctt
 660
 cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaataa
 717

<210> 22
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 22

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His Gln Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Phe Thr Thr Ser Thr Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 23
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 23

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His Gln Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 24
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 24

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His Asp Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Thr Lys Ala Asn Phe Gln Val Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys

225

230

235

<210> 25
 <211> 238
 <212> PRT
 <213> Aequora Victoria

<400> 25

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Asp His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 26
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 26

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His His Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 27
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 27

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His Val Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 28
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 28

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His Gln Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val

210

215

220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 29
 <211> 238
 <212> PRT
 <213> Aequora Victoria

<400> 29

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Asp His Thr Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 30
 <211> 238
 <212> PRT
 <213> Aequora Victoria
 <400> 30

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Asp His Leu Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Thr Lys Val Asn Phe Gln Val His His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 31
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 31

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His Asp Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Thr Lys Val Asn Phe Gln Val Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 32
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 32

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Asp His Leu Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Thr Lys Val Asn Phe Gln Val Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser

195

200

205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 33

<211> 238

<212> PRT

<213> Aequora Victoria

<400> 33

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Pro His Tyr Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Thr Lys Val Asn Phe Gln Val His His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 34
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 34

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Glu His Leu Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Thr Lys Ala Asn Phe Lys Ile His His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 35
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 35

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 36
<211> 238
<212> PRT
<213> Aequora Victoria

<400> 36

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Pro His Trp Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro

180					185					190					
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	His	Thr	Gln	Ser	Ala	Leu	Ser
	195						200					205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	210					215					220				
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
225					230					235					
<210>	37														
<211>	238														
<212>	PRT														
<213>	Aequora	Victoria													
<400>	37														
Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5					10					15	
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
			20					25					30		
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
		35					40					45			
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe
	50					55					60				
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70					75					80
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			100					105					110		
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115					120					125			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	130					135					140				
Tyr	Asn	Pro	His	Trp	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145					150					155					160
Thr	Lys	Val	Asn	Phe	Gln	Val	His	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				165					170					175	

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu His Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 38
<211> 238
<212> PRT
<213> Aequora Victoria

<220>
<221> MISC_FEATURE
<222> (93)..(93)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (95)..(95)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (147)..(147)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (149)..(149)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (166)..(166)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (168)..(168)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (202)..(202)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (204)..(204)
<223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (206)..(206)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (221)..(221)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (223)..(223)
 <223> Xaa = any amino acid

<400> 38

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Xaa Gln Xaa Arg
 85 90 95

Xaa Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Xaa His Xaa Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Xaa Ile Xaa His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Xaa Thr Xaa Ser Xaa Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Xaa Glu Xaa Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 39
 <211> 238
 <212> PRT
 <213> Aequora Victoria

<220>
 <221> MISC_FEATURE
 <222> (147)..(147)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (149)..(149)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (161)..(161)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (163)..(163)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (166)..(168)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (175)..(175)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (202)..(202)
 <223> Xaa = any amino acid

<400> 39

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Xaa His Xaa Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Xaa Lys Xaa Asn Phe Xaa Xaa Xaa His Asn Ile Glu Asp Gly Xaa Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Xaa Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235